

WEST[Help](#)[Logout](#)[Interrupt](#)[Main Menu](#)[Search Form](#)[Posting Counts](#)[Show S Numbers](#)[Edit S Numbers](#)[Preferences](#)**Search Results -**

Terms	Documents
13 same (conjugat\$ or fuse\$)	10

Database:

US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

Refine Search:

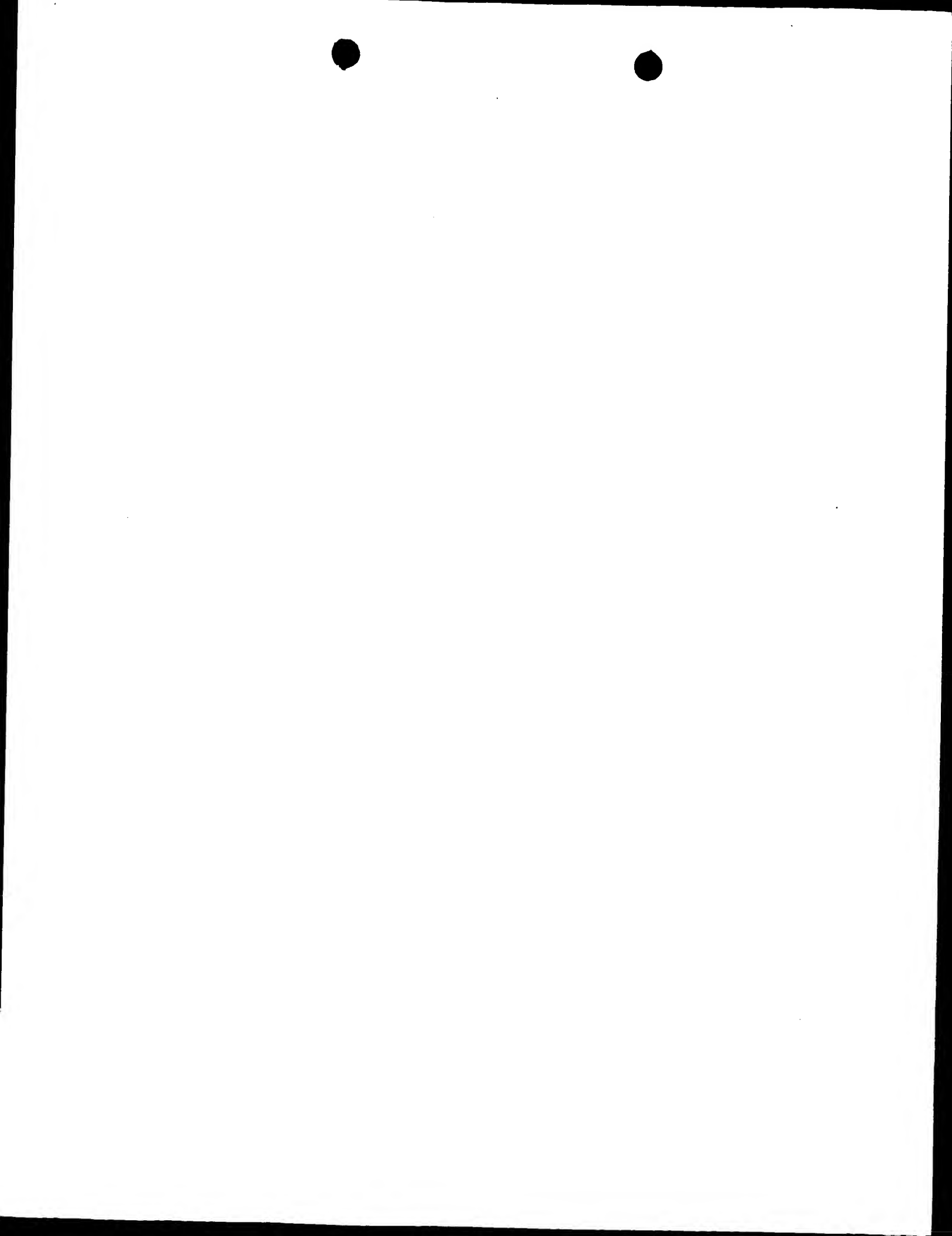
13 same (conjugat\$ or fuse\$)

[Clear](#)**Search History**

Today's Date: 1/17/2002

<u>DB Name</u>	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u>
USPT	13 same (conjugat\$ or fuse\$)	10	<u>L4</u>
USPT	12 same peptide\$	66	<u>L3</u>
USPT	albumin\$ same composition\$ same (stability or stable)	548	<u>L2</u>
USPT	fusion adj (protein\$ or polypeptide\$ or polypeptide\$)	12092	<u>L1</u>

09/424,080



(FILE 'HOME' ENTERED AT 12:50:47 ON 17 JAN 2002)

FILE 'MEDLINE' ENTERED AT 12:50:55 ON 17 JAN 2002
L1 128 S ALBUMIN (P) (STABILITY OR STABLE) (P) PEPTIDE?
L2 20 S L1 AND (FUSION? OR CONJUGATE?)
L3 20 DUP REM L2 (0 DUPLICATES REMOVED)

=>

09/424,080

1/17/02.

=> d his

(FILE 'HOME' ENTERED AT 13:45:18 ON 17 JAN 2002)
SET COST OFF

L1 FILE 'REGISTRY' ENTERED AT 13:45:27 ON 17 JAN 2002
L2 138 S LTEKKYSP/SQSP
1 S L1 AND 8/SQL

L3 FILE 'HCAOLD' ENTERED AT 13:45:45 ON 17 JAN 2002
0 S L2

L4 FILE 'HCAPLUS' ENTERED AT 13:45:48 ON 17 JAN 2002
1 S L2

L5 FILE 'USPATFULL, USPAT2' ENTERED AT 13:46:04 ON 17 JAN 2002
0 S L2

=> fil reg

FILE 'REGISTRY' ENTERED AT 13:46:19 ON 17 JAN 2002
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STRUCTURE FILE UPDATES: 15 JAN 2002 HIGHEST RN 383362-48-9
DICTIONARY FILE UPDATES: 15 JAN 2002 HIGHEST RN 383362-48-9

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES
for more information. See STNote 27, Searching Properties in the CAS
Registry File, for complete details:
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

=> d l2 sqide can

L2 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS
RN 216579-39-4 REGISTRY
CN L-Proline, L-leucyl-L-threonyl-L-.alpha.-glutamyl-L-lysyl-L-lysyl-L-
tyrosyl-L-seryl- (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE; STEREOSEARCH
SQL 8

SEQ 1 LTEKKYSP
=====

HITS AT: 1-8

MF C44 H72 N10 O14

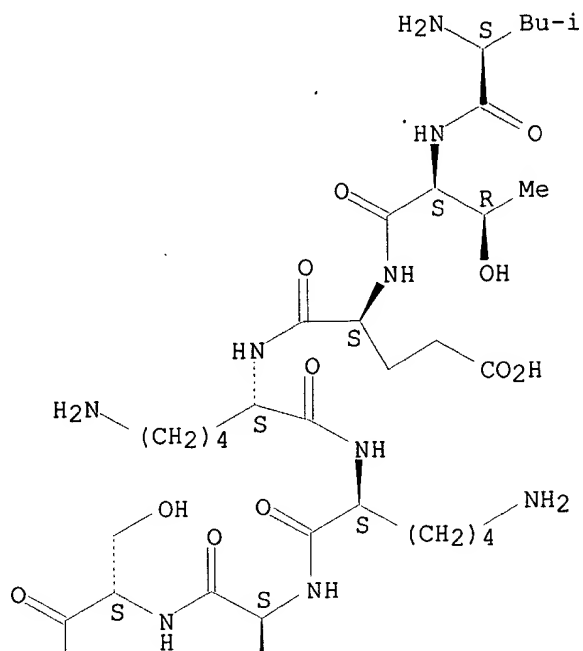
SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, TOXLIT

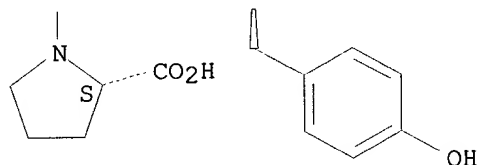
Absolute stereochemistry.

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

PAGE 1-A



PAGE 2-A



1 REFERENCES IN FILE CA (1967 TO DATE)
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 130:33014

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 13:46:26 ON 17 JAN 2002

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PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

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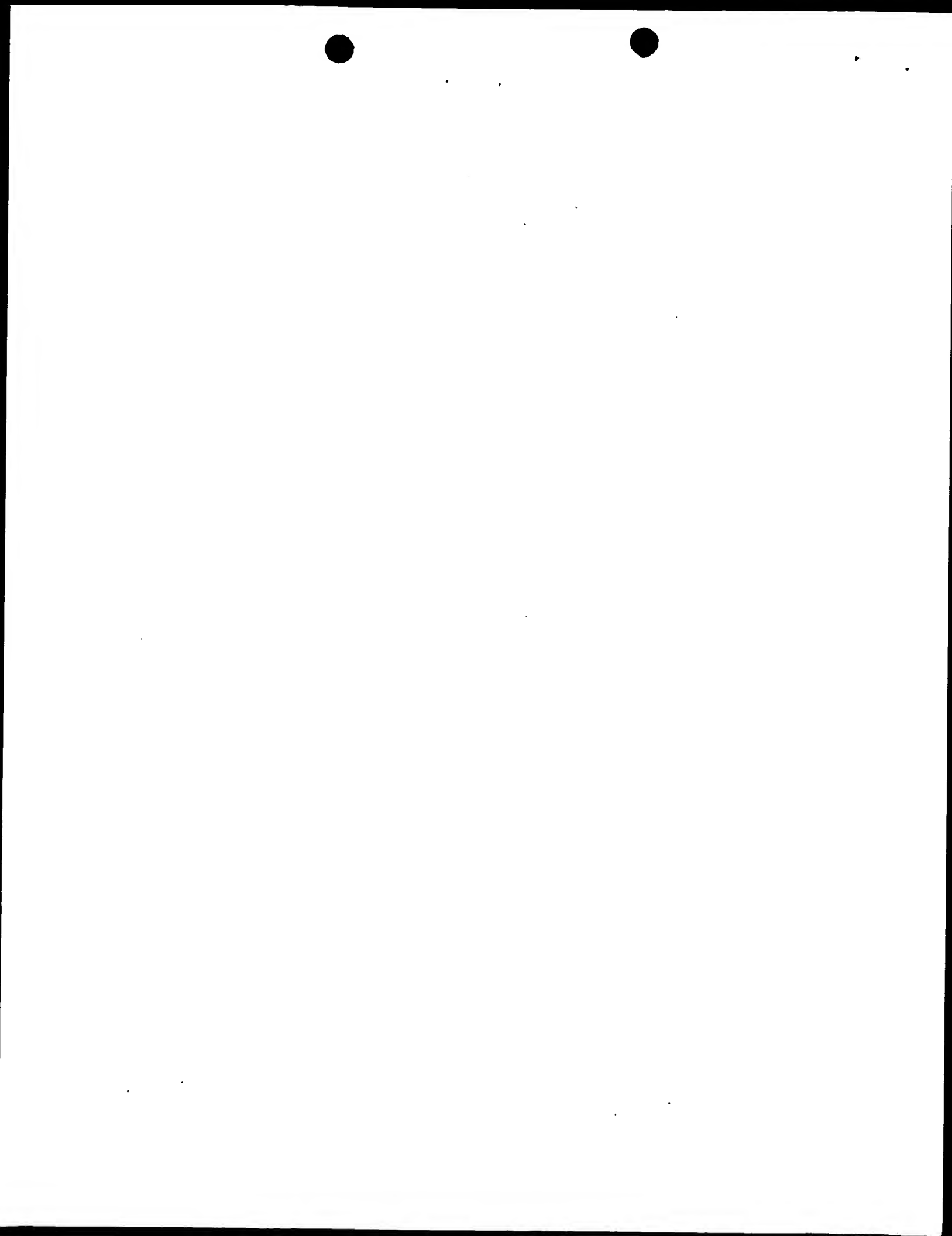
Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications.

FILE COVERS 1907 - 17 Jan 2002 VOL 136 ISS 3

FILE LAST UPDATED: 16 Jan 2002 (20020116/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REGISTRY for direct browsing and searching of



all substance data from the REGISTRY file. Enter HELP FIRST for more information.

HCAplus now provides online access to patents and literature covered in CA from 1907 to the present. Bibliographic information and abstracts were added in 2001 for over 3.8 million records from 1907-1966.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

=> d 14 all

L4 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
 AN 1998:789037 HCAPLUS
 DN 130:33014
 TI Compositions for enhancing immunosuppressants pharmaceutical activities
 IN Zavialov, Vladimir Petrovich; Vasilenko, Raisa Nikolaevna; Dolgikh, Dmitry Aleksandrovich; Kirpichnikov, Mikhail Petrovich; Navolotskaya, Elena Vitalievna; Korpela, Timo Kalevi
 PA Russia
 SO PCT Int. Appl., 26 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 IC ICM A61K038-04
 ICS A61K038-13; A61K038-21
 CC 1-7 (Pharmacology)
 Section cross-reference(s): 15
 FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9852594	A1	19981126	WO 1998-FI418	19980518
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
FI 9702121	A	19981120	FI 1997-2121	19970519
AU 9874352	A1	19981211	AU 1998-74352	19980518
EP 981359	A1	20000301	EP 1998-921528	19980518
R: AT, DE, ES, FR, GB, IT, SE, FI				
JP 2001526675	T2	20011218	JP 1998-550009	19980518
PRAI FI 1997-2121	A	19970519		
WO 1998-FI418	W	19980518		
AB	The present invention provides compns. for efficient amplification of immunosuppressive activity of cyclosporins, FK506 or rapamycin to decrease therapeutical dose of immunosuppressants and, as a consequence, avoidance of their undesirable side effects during organ and tissue transplantation, and treatment of different diseases. These compns. include cyclosporins, FK506 or rapamycin and biol. active peptides corresponding to the high-affinity binding/anti-lymphoproliferative site of IFNs-a,b,w,t, or recombinant proteins having the amino acid sequences corresponding to the said site.			
ST	immunosuppressant adjuvant formulation peptide			
IT	Interferon .tau. Interferon .alpha. Interferon .beta.			
RL:	PRP (Properties) (antilymphoproliferative site of; compns. for enhancing			

immunosuppressant pharmaceutical activities)

IT Adenocarcinoma inhibitors
Anti-inflammatory drugs
Antirheumatic drugs
Autoimmune diseases
Drug bioavailability
Immunosuppressants
Leukemia inhibitors
Lupus erythematosus
Lymphoma inhibitors
Myasthenia gravis
Psoriasis
Transplant (organ)
Uveitis
(comps. for enhancing immunosuppressant pharmaceutical activities)

IT Interferon .alpha.2
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(comps. for enhancing immunosuppressant pharmaceutical activities)

IT Peptides, biological studies
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(comps. for enhancing immunosuppressant pharmaceutical activities)

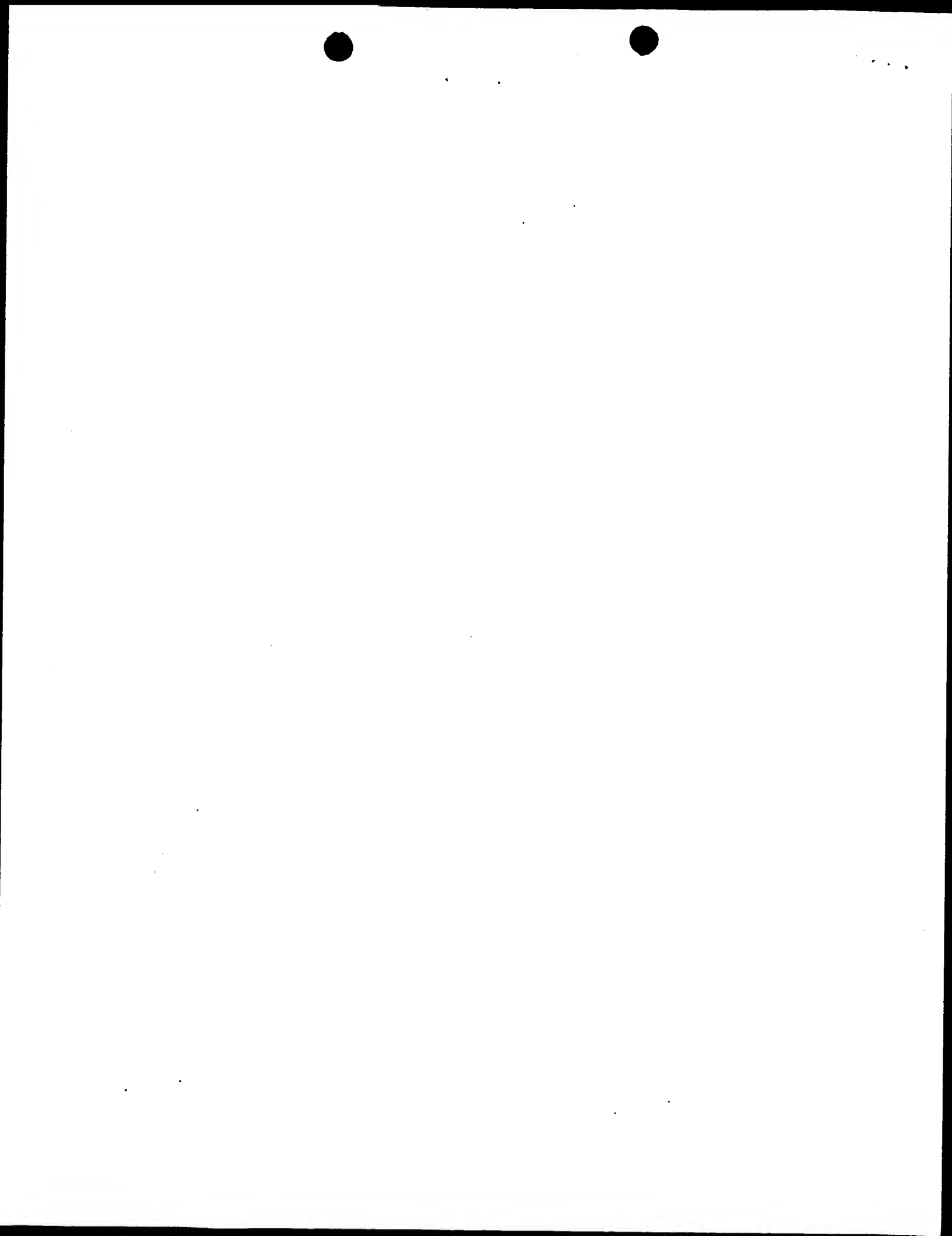
IT Interferons
RL: PRP (Properties)
(interferon .omega., antilymphoproliferative site of; comps. for enhancing immunosuppressant pharmaceutical activities)

IT Antitumor agents
(myeloma; comps. for enhancing immunosuppressant pharmaceutical activities)

IT 216579-39-4D, analogs 216579-44-1D, analogs
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(comps. for enhancing immunosuppressant pharmaceutical activities)

IT 53123-88-9, Rapamycin 79217-60-0D, Cyclosporin, derivs. 104987-11-3, Fk506
RL: PEP (Physical, engineering or chemical process); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(comps. for enhancing immunosuppressant pharmaceutical activities)

RE.CNT 5
RE
(1) University of Florida; WO 9009806 A2 1990 HCAPLUS
(2) University of Florida; WO 9410313 A2 1994 HCAPLUS
(3) Vacsyn, S; FR 2706772 A1 1994 HCAPLUS
(4) Zarogoulidis, K; Lung Cancer 1996, V15(2), P197 MEDLINE
(5) Zav'Yalov, V; Mol Immunol 1995, V32(6), P425 HCAPLUS



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OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:35 ; Search time 12.72 seconds

(without alignments)
47.909 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42

Sequence: 1 LTERKYSK 8

Scoring table: - BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 602

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	50.0	8	2	S21663
2	18	42.9	8	2	S11556
3	18	42.9	8	2	S15422
4	18	42.9	8	2	A58641
5	17	40.5	8	2	A05169
6	16	38.1	5	2	G37196
7	16	38.1	6	2	B44510
8	16	38.1	6	2	S20162
9	16	38.1	8	2	A14683
10	16	38.1	8	2	S45651
11	14	33.3	5	1	H0R0HA
12	14	33.3	5	2	A60411
13	14	33.3	7	2	PT0087
14	14	33.3	7	2	S09027
15	14	33.3	7	2	PD0029
16	14	33.3	8	2	A61348
17	14	33.3	8	2	S08995
18	14	33.3	8	2	A49823
19	14	33.3	8	2	A44960
20	14	33.3	8	2	A43976
21	14	33.3	8	2	B43976
22	14	33.3	8	2	S11545
23	14	33.3	8	2	D47393
24	13	31.0	7	2	PN0150
25	12	28.6	5	2	PQ0689
26	12	28.6	7	2	S17976
27	12	28.6	8	2	S16324
28	12	28.6	8	2	A23967
29	11	26.2	4	2	E44823

30	11	26.2	5	2	A41225
31	11	26.2	5	2	D60274
32	11	26.2	5	2	PT0714
33	11	26.2	6	2	A61411
34	11	26.2	6	2	A44916
35	11	26.2	6	2	A27696
36	11	26.2	6	2	PT0618
37	11	26.2	6	2	PT0715
38	11	26.2	6	2	A49421
39	11	26.2	7	2	A60139
40	11	26.2	7	2	E30608
41	11	26.2	7	2	S42620
42	11	26.2	7	2	I48086
43	11	26.2	7	2	PH0932
44	11	26.2	7	4	A58725
45	11	26.2	8	2	S08996

ALIGNMENTS

RESULT 1
S21663
neuropeptide - flower beetle (Pachnoda marginata)
C:Species: Pachnoda marginata
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S21663
R:Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
A:Title: Primary structures of neuropeptides isolated from the corpora cardiaca of va
electrometry.
A:Reference number: S21663; MUID:92265187
A:Accession: S21663
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <GAE>

Query Match 50.0%; Score 21; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKKYSP 8
DB 1 ELNYSK 6

RESULT 2
S11556
hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragmen
N:Alternate names: bisulfite reductase; desulfotuscidin
C:Species: Desulfovibrio thermophilus
C:Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C:Accession: S11556
R:Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DeVartanian, D.V.; Moura, J.J.G.
Biochim. Biophys. Acta 1040, 112-118, 1990
A:Title: Purification and characterization of bisulfite reductase (desulfotuscidin) f
A:Reference number: S11024; MUID:90335276
A:Accession: S11556
A:Molecule type: protein
A:Residues: 1-6 <FAU>
C:Keywords: oxidoreductase

Query Match 42.9%; Score 18; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKKY 6
DB 1:11
2 EKKY 5

RESULT 3

S15422

adipokine hormone - cockchafer

C:Species: Melolontha melolontha (cockchafer)

C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997

C:Accession: S15422

R:Gaede, G.

Biochem. J. 275, 671-677, 1991

A:Title: A unique charged tyrosine-containing member of the adipokine hormone/ red-pi

A:Reference number: S15422; MUID:91248100

A:Accession: S15422

A:Molecule type: protein

A:Residues: 1-8 <BIO>

C:Superfamily: adipokine hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 42.9%; Score 18; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 YSP 8

Db 4 YSP 6

RESULT 4

A58641

adipokine hormone - dor beetle

C:Species: Geotrupes stercoratus (dor beetle)

C:Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997

C:Accession: A58641

R:Gaede, G.

Biochem. J. 275, 671-677, 1991

A:Title: A unique charged tyrosine-containing member of the adipokine hormone/ red-pi

A:Reference number: S15422; MUID:91248100

A:Accession: A58641

A:Molecule type: protein

A:Residues: 1-8 <BIO>

C:Superfamily: adipokine hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 42.9%; Score 18; DB 2; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 YSP 8

Db 4 YSP 6

RESULT 5

A05169

neuropeptide M-1 - American cockroach

C:Species: Periplaneta americana (American cockroach)

C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993

C:Accession: A05169

R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.

Biochem. Biophys. Res. Commun. 124, 350-358, 1984

A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas

A:Reference number: A90118; MUID:85046550

A:Accession: A05169

A:Molecule type: protein

A:Residues: 1-8 <WTP>

C:Keywords: neuropeptide

Query Match

Best Local Similarity 40.5%; Score 17; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.2e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 EKKYSP 8

Db 1 EVNESP 6

RESULT 6

G37196

bradykinin-potentiating peptide 7 - island jararaca

C:Species: Bothrops insularis (island jararaca)

C:Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994

C:Accession: G37196

R:Chitra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptide

A:Reference number: A37196; MUID:90351557

A:Accession: G37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-5 <CTN>

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 38.1%; Score 16; DB 2; Length 5;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 KKYS 8

Db 1 QKNAP 5

RESULT 7

B44510

hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)

C:Species: Lactococcus lactis

C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993

C:Accession: B44510

R:Renault, P.; Gallard, C.; Heslot, H.

J. Bacteriol. 171, 3108-3114, 1989

A:Title: Product of the Lactococcus lactis gene required for malolactic fermentation

A:Reference number: A44510; MUID:89255069

A:Accession: B44510

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6 <REN>

A:Cross-references: EMBL:M90762

Query Match

Best Local Similarity 38.1%; Score 16; DB 2; Length 6;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 EKKY 6

Db 2 EKVY 5

RESULT 8

S20162

leghemoglobin III - Sesbania rostrata (fragment)

C:Species: Sesbania rostrata

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 04-Mar-2000

C:Accession: S20162

R:Metz, B.A.; Walters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.

Mol. Gen. Genet. 214, 181-191, 1988

A:Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-n

A:Reference number: S08322; MUID:89181515

A:Accession: S20162

A:Molecule type: DNA

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OM protein - protein search, using sw model

Run on: January 17, 2002, 12:15:20 ; Search time 10.03 Seconds
(without alignments)
29.244 Million cell updates/sec

Title: US-09-424-080A-1

Perfect score: 42
Sequence: 1 LTERKXSP 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 138

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	19	45.2	8	UH09_RAT	P56575 ratnus norv
2	18	42.9	8	AKH_MELML	P25423 melolontha
3	16	38.1	5	BPP7_BOTIN	P30425 botinops in
4	14	33.3	5	PRCT_PERAM	P01373 periplaneta
5	14	33.3	6	ASP2_LACSN	P82655 lactobacill
6	14	33.3	6	OVM_LBPPD	P42985 leptinotars
7	14	33.3	8	ALL4_CAYVO	P41840 calliphora
8	14	33.3	8	HTFL_PERAM	P25419 tenebrio mo
9	14	33.3	8	HTFL_TENMO	P08933 pandalus bo
10	14	33.3	8	RPCH_PANBO	P22396 locusta mig
11	13	31.0	8	LMT2_LOCM1	P42564 hirtudo medi
12	12	28.6	7	ALL7_CARMA	P81820 carcius ma
13	12	28.6	8	ALL3_CYDPO	P82154 cydia pomon
14	12	28.6	8	ALL4_CYDPO	P82155 cydia pomon
15	12	28.6	8	ALL4_CYDPO	P82155 cydia pomon
16	12	28.6	8	ALL4_CYDPO	P82155 cydia pomon
17	11	26.2	5	ALL4_CARMA	P81817 carcius ma
18	11	26.2	6	CIP1_MYTED	P32310 herpes simp
19	11	26.2	7	VP19_HSVIK	P82158 cydia pomon
20	11	26.2	7	ALL7_CYDPO	P25418 libellula a
21	11	26.2	8	AKH_TYBAT	P14595 tabanus atr
22	11	26.2	8	AKH_TYBAT	P81818 carcius ma
23	11	26.2	8	AKH_TYBAT	P81819 carcius ma
24	11	26.2	8	AKH_TYBAT	P81821 carcius ma
25	11	26.2	8	AKH_TYBAT	P81821 carcius ma
26	11	26.2	8	AKH_TYBAT	P81821 carcius ma
27	11	26.2	8	AKH_TYBAT	P81821 carcius ma
28	11	26.2	8	AKH_TYBAT	P81821 carcius ma
29	11	26.2	8	AKH_TYBAT	P81821 carcius ma
30	11	26.2	8	AKH_TYBAT	P81821 carcius ma
31	10	23.8	7	IGAO_DACDE	P06294 dactylium d
32	10	23.8	8	FAR4_HOMAM	P4187 homarus ame
33	10	23.8	8	NPB_BOVIN	P15507 bos taurus

34	9	21.4	5	1	FARP_ARTTR	P41853 artiposthi
35	9	21.4	7	1	MSCL_SALTZ	P39446 salmonella
36	9	21.4	7	1	OC24_MAIZE	P80630 zea mays (m
37	9	21.4	7	1	WMA2_ACHPU	P35920 achattina fu
38	9	21.4	7	1	WMA3_ACHPU	P35921 achattina fu
39	9	21.4	8	1	ACT_THUAL	P18691 thunnus alb
40	9	21.4	8	1	AMG2_BORTA	P10582 bolitops ja
41	9	21.4	8	1	B4AK_FOKSI	P1886 porphyromon
42	9	21.4	8	1	UPAA_HUMAN	P30096 homo sapien
43	8	19.0	4	1	RM01_YEAST	P26515 saccharomyc
44	8	19.0	5	1	PAV2_PARMA	P81864 parachitrus
45	8	19.0	5	1	PSK_DAUCA	P8261 daucus caro

ALIGNMENTS

RESULT 1
ID UH09_RAT STANDARD: PRT: 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P9) (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=WISTAR; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.; Submitted (SEP-1998) to the SWISS-PROT data bank.
RL Submitted (SEP-1998) ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 KDA.
FT NON-TER
SQ SEQUENCE 8 AA: 1029 MW: 9E0775A6CA140B06 CRC64;

Query Match 45.2% Score 19; DB 1; Length 8;
Best Local Similarity 50.0% Pred. No. 1e+05; 1; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 1;
QY 3 EKKYSP 8
Db 2 ERKSP 7
RESULT 2
ID AKH_MELML STANDARD: PRT: 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ADIPOKINETIC HORMONE (AKH).
OS Melolontha melolontha (Cockchafer).
OS Geotrupes stercorosus (Dor beetle), and
OS Pterodroma marginata (Pterodroma);
OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
OX NCBI_TaxID=7061, 7087, 7058;
RN [1]
RP SEQUENCE.
RC SPECIES=M.melolontha, and G.stercorosus; TISSUE=Corpora cardiaca;
RX MEDLINE=91248100; Pubmed=2039445;
RA Gaede G.;
RT "A unique charged tyrosine-containing member of the adipokinetin
hormone/red-pigment-concentrating hormone peptide family isolated and
sequenced from two beetle species.";

RL Biochem. J. 275:671-677(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-P. marginata; TISSUE-Corpus cardiaca;
 RX MEDLINE-926518; Pubmed-1586453;
 RA Gade G., Lopata A., Kellner R., Rinehart K.L. Jr.;
 RT "Primary structures of neuropeptides isolated from the corpora
 RT cardiaca of various cetoid beetle species determined by
 RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
 RT spectrometry."
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 CC PIR: S15422; S15422.
 CC PIR: S21663; S21663.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD. RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 FT MOD. RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1022 MW; 867AB75AB544736 CRC64;

Query Match 42.9%; Score 18; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 YSP 8
 111
 DB 4 YSP 6

RESULT 3
 BPP7_BOTIN STANDARD; PRT; 5 AA.
 AC P30425;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE BRADYKININ-POTENTIATING PEPTIDE S5.2 (5A) (ANGIOTENSIN-CONVERTING
 DE ENZYME INHIBITOR).
 OS Bothrops insularis (Island jararaca) (Oueimada jararaca).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Viperidae; Crotalinae; Bothrops.
 NC NCB1_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE-90351557; Pubmed-2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom."
 RL J. Protein Chem. 9:221-227(1990).
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR: G37196; G37196.
 KW Hypotensive agent; Venom.
 FT MOD. RES 1 1 PYROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 38.1%; Score 16; DB 1; Length 5;
 Best Local Similarity 40.0%; Pred. No. 1e+05;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 KRYSP 8
 1111

DB 1 OKMAP 5
 RESULT 4
 PROCT_PERAM STANDARD; PRT; 5 AA.
 ID PROCT_PERAM
 AC P01373;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE PROCTOLIN.
 OS Periplaneta americana (American cockroach),
 OS Limulus polyphemus (Atlantic horseshoe crab), and
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattella; Periplaneta.
 CC NCB1_TaxID=6978; 6850, 6759;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-P. americana;
 RX MEDLINE-76074708; Pubmed-576;
 RA Starratt A.N., Brown B.E.;
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 RT in insects."
 RL Life Sci. 17:1253-1256(1975).
 RN [2]
 RP BIOLOGICAL SOURCE.
 RC SPECIES-P. americana;
 RX MEDLINE-81225865; Pubmed-6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron."
 RL Science 213:567-569(1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES-L. polyphemus;
 RX MEDLINE-90287800; Pubmed-2356151;
 RA Groome J.R., Tillingshast E.K., Townley M.A., Velours A.,
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 RT horseshoe crab, Limulus polyphemus."
 RL Peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES-C. maenas;
 RX MEDLINE-86232789; Pubmed-2872661;
 RA Stangier J., Dirksen H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 RT pericardial organs of the shore crab, Carcinus maenas."
 RL Peptides 7:67-72(1986).
 CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 CC PIR: A01644; HOROHA.
 DR PIR: A60411; A60411.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 33.3%; Score 14; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 KYSP 8
 1111
 DB 1 KYSP 4

RESULT 5
 ASP2_LACSN STANDARD; PRT; 6 AA.
 ID ASP2_LACSN

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OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:50 ; Search time 22.03 Seconds
(without alignments)
53.118 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTKKYSR 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 352

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	59.5	8	2	Q9R9E0 bacillus su
2	14	33.3	7	13	P82101 ilitoria rub
3	14	33.3	8	8	Q9TMM4 begonia for
4	14	33.3	8	8	Q9TMM4 begonia tai
5	14	33.3	8	8	Q9TMM4 begonia apt
6	14	33.3	8	10	Q9XGL8 begonia nan
7	14	33.3	8	10	Q9XGL8 begonia pal
8	14	33.3	8	10	Q9XGL8 begonia pal
9	13	31.0	8	12	Q9R7T2 escherichia
10	13	31.0	8	12	Q9R7T2 escherichia
11	12	28.6	8	8	Q9XSY1 canis famill
12	12	28.6	8	8	Q9XSY1 canis famill
13	12	28.6	8	11	Q63933 rattus norv
14	12	26.2	7	2	Q54248 streptomyces
15	11	26.2	8	2	Q56429 thermus aqu
16	11	26.2	8	2	Q9R5L7 clostridium
17	11	26.2	8	4	Q15895 homo sapien
18	11	26.2	8	5	P82689 periplaneta
19	11	26.2	8	6	P82929 bos taurus

20	11	26.2	8	6	Q9BFA7	Q9BFA7 macrocellid
21	11	26.2	8	7	Q95213	Q95213 oryctolagus
22	11	26.2	8	8	Q9T2Y3	Q9T2Y3 begonia for
23	10	23.8	6	10	P82541	P82541 psathirosta
24	10	23.8	7	8	P92385	P92385 hordeum mar
25	10	23.8	7	8	P92210	P92210 agropyron c
26	10	23.8	7	8	P92214	P92214 amblyopyrum
27	10	23.8	7	8	P92218	P92218 australopyr
28	10	23.8	7	8	P92221	P92221 bromus iner
29	10	23.8	7	8	P92226	P92226 crithopsis
30	10	23.8	7	8	P92372	P92372 haynaldia v
31	10	23.8	7	8	P92381	P92381 hordeum bra
32	10	23.8	7	8	P92387	P92387 henrardia p
33	10	23.8	7	8	P92390	P92390 heteranthel
34	10	23.8	7	8	P92393	P92393 hordeum vul
35	10	23.8	7	8	P92425	P92425 pseudoroegn
36	10	23.8	7	8	P92427	P92427 peridictyon
37	10	23.8	7	8	P92430	P92430 aegilops ta
38	10	23.8	7	8	P92430	P92430 taenialtheru
39	10	23.8	7	8	P92440	P92440 thionopyrum
40	10	23.8	7	8	P92440	P92440 thionopyrum
41	10	23.8	7	8	P92403	P92403 lophopyrum
42	10	23.8	7	12	O66205	O66205 porcine lra
43	10	23.8	8	2	O44463	O44463 agrobacteri
44	10	23.8	8	2	O92IE9	O92IE9 neisseria m
45	10	23.8	8	2	Q9R5R0	Q9R5R0 shigella dy

ALIGNMENTS

RESULT 1
ID Q9R9E0 PRELIMINARY: PRT: 8 AA.
AC Q9R9E0:
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)
DE STAGE V SPORULATION PROTEIN E (FRAGMENT).
GN SPOVE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP STRAIN=168;
RX MEDLINE=93003529; PubMed=1391053;
RA Henriques A.O., de Lencastre H., Pigot P.J.;
RT "A Bacillus subtilis morphogene cluster that includes spoVE is homologous to the mra region of Escherichia coli.";
RL Biochimie 74:735-748(1992).
DR EMBL; X64258; CAA45556.1; -.
FT NON_TER
SQ SEQUENCE 8 AA: 893 MW; EE75A1A33321B1A6 CRC64;

Query Match 59.5%; Score 25; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.7e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTKKYSR 8
: | | | |
Db 1 MTKTKRSP 8
RESULT 2
ID P82101 PRELIMINARY: PRT: 7 AA.
AC P82101:
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)

DE ELECTRIN 5.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;
 RA Mambitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella".
 RL Aust. J. Chem. 52:0-0(1999).
 KW Amphibian skin; Amidation.
 FT MOD_RES
 SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 33.3%; Score 14; DB 13; Length 7;
 Best Local Similarity 66.7%; Pred. No. 4.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TEKK 8
 Db 2 YEP 4

RESULT 3
 ID 097MNA PRELIMINARY; PRT; 8 AA.
 AC 097MNA;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE RBCL PROTEIN (FRAGMENT).
 GN RBCL.
 OS Begonia formosana.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Cucurbitales; Begoniaceae; Begonia.
 OX NCBI_TaxID=80370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chiang T.Y.;
 RT "Sequence announcement: rbcl promoter gene in Begonia formosana."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 UR EMBL; AJ009597; CAB52119.1;
 KM Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;

Query Match 33.3%; Score 14; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 4.7e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TEKK 5
 Db 5 TEKK 8

RESULT 4
 ID 0972Y2 PRELIMINARY; PRT; 8 AA.
 AC 0972Y2;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE RBCL PROTEIN (FRAGMENT).
 GN RBCL.
 OS Begonia taipeiensis.

OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids I; Cucurbitales; Begoniaceae; Begonia.
 OX NCBI_TaxID=80371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chiang T.Y.;
 RT "Sequence announcement: rbcl promoter gene in Begonia formosana."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ009602; CAB52129.1;
 DR EMBL; AJ009600; CAB52125.1;
 DR EMBL; AJ009601; CAB52127.1;
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;

Query Match 33.3%; Score 14; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 4.7e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TEKK 5
 Db 5 TEKK 8

RESULT 5
 ID 0972Y1 PRELIMINARY; PRT; 8 AA.
 AC 0972Y1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE RBCL PROTEIN (FRAGMENT).
 GN RBCL.
 OS Begonia aptera.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC eurosids I; Cucurbitales; Begoniaceae; Begonia.
 OX NCBI_TaxID=71278;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chiang T.Y.;
 RT "Sequence announcement: rbcl promoter gene in Begonia formosana."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ009606; CAB52086.1;
 DR EMBL; AJ009603; CAB52080.1;
 DR EMBL; AJ009604; CAB52082.1;
 DR EMBL; AJ009605; CAB52084.1;
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 8 AA; 921 MW; FA21AB01B6C775B6 CRC64;

Query Match 33.3%; Score 14; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 4.7e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TEKK 5
 Db 5 TEKK 8

RESULT 6
 ID 09XG19 PRELIMINARY; PRT; 8 AA.
 AC 09XG19;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DE ATPB PROTEIN (FRAGMENT).

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OM protein - protein search, using sw model

Run on: January 17, 2002, 12:12:40 ; Search time 23.54 Seconds
(without alignments)
25.174 Million cell updates/sec

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Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTEKKYSP 8
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 segs, 74073290 residues
total number of hits satisfying chosen parameters: 62388

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Minimum DB seq length: 0
Maximum DB seq length: 8
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :

A_Geneseq_1101.*

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- 2: /SIDB8/gcgdata/geneseq/geneseq/Aa1981.DAT: *
- 3: /SIDB8/gcgdata/geneseq/geneseq/Aa1982.DAT: *
- 4: /SIDB8/gcgdata/geneseq/geneseq/Aa1983.DAT: *
- 5: /SIDB8/gcgdata/geneseq/geneseq/Aa1984.DAT: *
- 6: /SIDB8/gcgdata/geneseq/geneseq/Aa1985.DAT: *
- 7: /SIDB8/gcgdata/geneseq/geneseq/Aa1986.DAT: *
- 8: /SIDB8/gcgdata/geneseq/geneseq/Aa1987.DAT: *
- 9: /SIDB8/gcgdata/geneseq/geneseq/Aa1988.DAT: *
- 10: /SIDB8/gcgdata/geneseq/geneseq/Aa1989.DAT: *
- 11: /SIDB8/gcgdata/geneseq/geneseq/Aa1990.DAT: *
- 12: /SIDB8/gcgdata/geneseq/geneseq/Aa1991.DAT: *
- 13: /SIDB8/gcgdata/geneseq/geneseq/Aa1992.DAT: *
- 14: /SIDB8/gcgdata/geneseq/geneseq/Aa1993.DAT: *
- 15: /SIDB8/gcgdata/geneseq/geneseq/Aa1994.DAT: *
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- 17: /SIDB8/gcgdata/geneseq/geneseq/Aa1996.DAT: *
- 18: /SIDB8/gcgdata/geneseq/geneseq/Aa1997.DAT: *
- 19: /SIDB8/gcgdata/geneseq/geneseq/Aa1998.DAT: *
- 20: /SIDB8/gcgdata/geneseq/geneseq/Aa1999.DAT: *
- 21: /SIDB8/gcgdata/geneseq/geneseq/Aa2000.DAT: *
- 22: /SIDB8/gcgdata/geneseq/geneseq/Aa2001.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	26	61.9	6	15	AA059059	Peptide signal seq
2	24	57.1	6	21	AA036378	Rat SM/IM/CRP2
3	24	57.1	6	22	AA005552	NLS of rat smooth
4	24	57.1	7	20	AA095356	Human IgG4 upper h
5	24	57.1	7	22	AA061834	Human Ig gamma4
6	24	57.1	8	16	AA021215	Farnesyl synthetas
7	24	57.1	8	14	AA021716	Farnesyl synthetas
8	21	50.0	8	20	AA036135	Hepatitis C virus
9	21	50.0	8	20	AA008147	Clotting factor VII
10	21	50.0	8	20	AA008148	Clotting factor VII
11	21	50.0	8	20	AA008149	Clotting factor VI

12	21	50.0	8	20	AA808150
13	20	47.6	5	22	AA82021
14	20	47.6	7	17	AA802186
15	20	47.6	7	19	AA859328
16	20	47.6	7	20	AA850085
17	20	47.6	7	21	AA809693
18	20	47.6	7	22	AA800685
19	20	47.6	7	22	AA800686
20	20	47.6	7	22	AA800953
21	20	47.6	7	22	AA8E00956
22	20	47.6	7	22	AA846124
23	20	47.6	7	22	AA849441
24	20	47.6	8	16	AA879692
25	20	47.6	8	18	AA893531
26	20	47.6	8	20	AA8199730
27	20	47.6	8	21	AA857993
28	19	45.2	5	22	AA804832
29	19	45.2	6	19	AA846584
30	19	45.2	6	22	AA805500
31	19	45.2	7	17	AA806266
32	19	45.2	7	18	AA843301
33	19	45.2	7	18	AA834282
34	19	45.2	7	20	AA814763
35	19	45.2	7	20	AA895148
36	19	45.2	7	21	AA801902
37	19	45.2	7	22	AA804479
38	19	45.2	8	15	AA872419
39	19	45.2	8	16	AA879693
40	19	45.2	8	17	AA805444
41	19	45.2	8	20	AA847205
42	19	45.2	8	20	AA844894
43	19	45.2	8	20	AA810292
44	19	45.2	8	20	AA894115
45	19	45.2	8	21	AA833455

ALIGNMENTS

RESULT

AAR59959 standard; peptide; 6 AA.

AAR59959

14-FEB-1995 (first entry)

Peptide signal sequence for treating leukocyte interferon diseases.

Therapeutic; metabolic interactions; PSS; analogues

Synthetic.

W09416328-A.

21-JUL-1994

30-DEC-1993; 93WO-US12679.

30-DEC-1992; 92US-0997727.

(RATH/) RATH M.

Rath M;

WPI; 1994-249399/30.

Identifying peptide signal sequences in a protein - and use of their synthetic analogues for treating or preventing, e.g. cardiovascular and auto-immune disease, infections and cancer.

Claim 29; Page 14; 28pp; English

CC The sequence is that of a peptide signal sequence which can be used
 CC to treat diseases involving human leucocyte interferons, including
 CC cancer, immunodeficiencies and infectious diseases.
 CC See also AAB59944-83.

XX Sequence 6 AA;

Query Match 61.9%; Score 26; DB 15; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 EKYS 7
 |||||
 Db 2 ekys 6

RESULT 2

AAB36378
 ID AAB36378 standard; Peptide: 6 AA.

AC AAB36378;

DE 27-FEB-2001 (first entry)

DE Rat SMLIM/CRP2 putative nuclear localisation signal SEQ ID NO:15.

KM Hypertension; inhibition; treatment; SMLIM; CRP; LIM domain;

XX smooth muscle cell LIM; vascular smooth muscle cell; hypotensive.

OS Rattus sp.

PN WO200066734-A1.

PD 09-NOV-2000.

PF 05-MAY-2000; 2000MO-US12189.

PR 05-MAY-1999; 9905-0305839.

PA (HARD) HARVARD COLLEGE.

PI Lee M, Yet S;

WPI; 2000-687540/67.

PT Novel nucleic acid encoding a regulatory sequence which acts
 PT preferentially in vascular smooth muscle cells, operatively linked to
 PT an antisense template, used to treat hypertension -

XX Disclosure; Page 33; 91pp; English.

CC The present invention describes a nucleic acid, comprising a sequence
 CC at least 50 % identical to a mouse SMLIM/CRP promoter cis-acting
 CC regulatory sequence, operably linked to an antisense template
 CC complementary to part of an mRNA encoding a vascular smooth muscle cell
 CC polypeptide. The first sequence directs expression of the second
 CC preferentially in vascular smooth muscle cells. Also described are:
 CC (1) screening candidate compounds to identify a compound capable of
 CC decreasing expression of SMLIM/CRP2 in vascular smooth muscle cells,
 CC comprising: (a) contacting a vascular smooth muscle cell with a
 CC candidate compound; and (b) determining the amount of SMLIM/CRP2
 CC expression in the cell; and (2) a transgenic non-human mammal, the
 CC germ cells and somatic cells of which comprise a null mutation in a
 CC gene encoding SMLIM. The nucleic acids can be used for identifying
 CC compounds that decrease expression of SMLIM/CRP2 in vascular smooth
 CC muscle cells. Compounds that reduce the expression of SMLIM can be
 CC used to decrease hypertension in mammals. Compounds that reduced SMLIM
 CC activity can be used to inhibit hypertension in mammals. AAC64704 to
 CC AAC64723 and AAB36370 to AAB36384 represent sequences used in the
 CC exemplification of the present invention.

XX Sequence 6 AA;

Query Match 57.1%; Score 24; DB 21; Length 6;
 Best Local Similarity 80.0%; Pred. No. 4.3e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 KKYS 8
 |||||
 Db 1 kkys 5

RESULT 3

AAE05552
 ID AAE05552 standard; peptide: 6 AA.

AC AAE05552;

DE 24-SEP-2001 (first entry)

DE NLS of rat smooth muscle cell LIM (SMLIM/CRP2) protein.

KM Rat; smooth muscle cell LIM; SMLIM/CRP2 protein; arteriosclerosis;

KM neointima formation; balloon angioplasty; vascular disease; cardiac;

KM angiogenesis; peripheral vascular disease; coronary artery disease;

XX gene therapy; antisense therapy; nuclear localisation signal; NLS.

OS Rattus sp.

PN US6258557-B1.

PD 10-JUL-2001.

PF 14-MAR-1997; 97US-0818655.

PR 15-MAR-1996; 96US-0616368.

PA (HARD) HARVARD COLLEGE.

PI Lee M, Haber E, Jain M, Yet S;

WPI; 2001-450366/48.

PT Isolated DNA encoding smooth muscle cell LIM (SMLIM/CRP2) useful for
 PT inhibiting arterial smooth muscle proliferation and for treating
 PT peripheral vascular disease, arteriosclerosis and coronary artery
 PT disease -

XX Disclosure; Column 19; 38pp; English.

CC The invention relates to an isolated DNA which regulates vascular
 CC smooth muscle cell-specific transcription of a polypeptide-encoding
 CC sequence to which it is operably linked. The invention is based on
 CC the identification and characterisation of a smooth muscle cell LIM
 CC (SMLIM/CRP2) polypeptide which is expressed preferentially in arterial
 CC smooth muscle cells. SMLIM/CRP2 sequence is useful for directing
 CC vascular smooth muscle cell-specific expression of a polypeptide, by
 CC introducing vector comprising SMLIM/CRP2 into a vascular smooth muscle
 CC cell and maintaining cell under conditions suitable for polypeptide
 CC expression. SMLIM/CRP2 is useful for inhibiting arterial smooth muscle
 CC proliferation and for inhibiting neointima formation after balloon
 CC angioplasty. SMLIM/CRP2 nucleotide sequence is useful for increasing
 CC the level of SMLIM/CRP2 polypeptide in injured vascular tissues for
 CC inhibiting proliferation of smooth muscle cells. SMLIM/CRP2 is useful
 CC in gene therapy and antisense therapy for treating vascular diseases
 CC such as arteriosclerosis, and to promote angiogenesis to treat diseases
 CC present sequence is nuclear localisation signal (NLS) of rat smooth
 CC muscle cell LIM (SMLIM/CRP2) protein.

XX Sequence 6 AA;

Query Match 57.1%; Score 24; DB 22; Length 6;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2002, 12:14:15 ; Search time 12.51 Seconds
(without alignments)
14.391 Million cell updates/sec

Title: US-09-424-080A-1
Perfect score: 42
Sequence: 1 LTERKYSF 8

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 43125

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents_AA:
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	8	2	US-08-669-284B-30
2	26	61.9	6	5	PCT-US93-12679-16
3	24	57.1	6	1	US-08-616-368A-15
4	24	57.1	6	4	US-09-054-298-15
5	24	57.1	6	4	US-08-818-655-15
6	24	57.1	6	4	US-08-891-271-13
7	22	52.4	7	3	US-08-756-849-123
8	21	50.0	8	4	US-08-444-818-659
9	20	47.6	7	3	US-08-390-353A-9
10	20	47.6	7	4	US-09-371-710-48
11	20	47.6	7	4	US-09-147-933-31
12	20	47.6	7	4	US-08-862-124-26
13	20	47.6	7	4	US-08-862-124-26
14	20	47.6	7	4	US-09-648-386-48
15	20	47.6	8	1	US-08-178-570-47
16	20	47.6	8	3	US-08-369-643-47
17	20	47.6	8	5	PCT-US95-00147-47
18	19	45.2	6	2	US-08-676-378-8
19	19	45.2	7	1	US-07-638-497-15
20	19	45.2	7	3	US-08-604-965E-10
21	19	45.2	7	3	US-08-604-965E-10
22	19	45.2	7	6	5258287-43
23	19	45.2	8	1	US-08-178-570-48
24	19	45.2	8	3	US-08-369-643-48
25	19	45.2	8	5	PCT-US95-00147-48
26	19	45.2	8	6	5258287-44
27	18	42.9	5	2	US-08-928-958-20

28	18	42.9	5	2	US-09-072-429-20	Sequence 20, Appl
29	18	42.9	6	1	US-08-082-847-13	Sequence 13, Appl
30	18	42.9	6	2	US-08-928-958-21	Sequence 21, Appl
31	18	42.9	6	2	US-09-072-429-21	Sequence 21, Appl
32	18	42.9	6	2	US-09-127-574-17	Sequence 17, Appl
33	18	42.9	6	4	US-09-171-654-70	Sequence 70, Appl
34	18	42.9	6	4	US-09-496-379-10	Sequence 10, Appl
35	18	42.9	6	4	US-09-496-379-10	Sequence 11, Appl
36	18	42.9	7	1	US-08-082-847-17	Sequence 25, Appl
37	18	42.9	7	1	US-08-082-847-25	Sequence 11, Appl
38	18	42.9	7	1	US-08-218-027A-1	Sequence 2, Appl
39	18	42.9	7	1	US-08-218-027A-2	Sequence 4, Appl
40	18	42.9	7	1	US-08-218-027A-4	Sequence 6, Appl
41	18	42.9	7	1	US-08-218-027A-6	Sequence 7, Appl
42	18	42.9	7	1	US-08-218-027A-7	Sequence 7, Appl
43	18	42.9	7	1	US-08-040-548-40	Sequence 40, Appl
44	18	42.9	7	1	US-08-466-344-40	Sequence 40, Appl
45	18	42.9	7	1	US-08-466-344-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-08-669-284B-30
Sequence 30, Application US/08669284B
Patent No. 5939534
GENERAL INFORMATION:
APPLICANT: Inoue, Makoto
APPLICANT: Kikuchi, Kaoru
APPLICANT: Ishige, Yoko
APPLICANT: Ito, Akira
APPLICANT: Kimura, Toru
APPLICANT: Nakayama, Chikao
APPLICANT: No. 5939534uchi, Hiroshi
TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUTROTROPIC FACTORS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: SUGHRUE, MION, ZINN, MACPHEE & SEAS
ADDRESS: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,284B
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/02269
FILING DATE: 27-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-268281
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 06-201504
FILING DATE: 02-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-350934
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: O-42041
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-284B-30

Query Match 100.0%; Score 42; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKKXSP 8
Db 1 LTKKXSP 8

RESULT 2

PCT-US93-12679-16
Sequence 16, Application PC/TUS9312679
GENERAL INFORMATION:
APPLICANT: Rath, Mathias
TITLE OF INVENTION: SYNTHETIC OLIGOPEPTIDES ANALOGOUS TO
TITLE OF INVENTION: PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHELDON & MAK
STREET: 401 Florence Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12679
FILING DATE: 30-DEC-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Cranfill, Raymond B
REGISTRATION NUMBER: 32,845
REFERENCE/DOCKET NUMBER: RATH-10016PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5333
TELEFAX: 415-322-5499
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-12679-16

Query Match 61.9%; Score 26; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EKXYS 7
Db 2 EKXYS 6

RESULT 3

US-08-616-368A-15
Sequence 15, Application US/08616368A
Patent No. 5767262
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En

APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,368A
FILING DATE: 15-MAR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/022001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-616-368A-15

Query Match 57.1%; Score 24; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KXKSP 8
Db 1 KXKSP 5

RESULT 4

US-09-054-298-15
Sequence 15, Application US/09054298
Patent No. 6136953
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,298

FILING DATE: 02-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Beattie, Ph.D., Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 05433/022002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-054-298-15

Query Match 57.1%; Score 24; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRYSP 8
1111
Db 1 KRYGP 5

RESULT 5
US-08-818-655-15
Sequence 15, Application US/08818655
Patent No. 6258557
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Yel, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,655
FILING DATE: 14-MAR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-818-655-15

Query Match 57.1%; Score 24; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KRYSP 8
1111
Db 1 KRYGP 5

RESULT 6
US-08-891-271-13
Sequence 13, Application US/08891271
Patent No. 6165476
GENERAL INFORMATION:
APPLICANT: Strom, Terry B.
APPLICANT: Sytkowski, Arthur J.
APPLICANT: Zheng, Xia Xiao
TITLE OF INVENTION: Fusion Proteins with an Immunoglobulin
TITLE OF INVENTION: Hing Region Linker
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,271
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hogle, Doreen M.
REGISTRATION NUMBER: 36,361
REFERENCE/DOCKET NUMBER: BIH97-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-891-271-13

Query Match 57.1%; Score 24; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKRYP 8
1111
Db 1 ESKYGP 6

RESULT 7
US-08-756-849-123
Sequence 123, Application US/08756849
Patent No. 6093810
GENERAL INFORMATION:
APPLICANT: Bird, David M.K.
APPLICANT: Wilson, Mark A.
TITLE OF INVENTION: Nematode-Induced Genes in Tomato

NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,849
FILING DATE: 26-NOV-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,474
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-05351005
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-756-849-123

Query Match 52.4%; Score 22; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TEKKISP 8
| | |
Db 1 TSPSYSP 7

RESULT 8
US-08-444-818-659
Sequence 559, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Butler, William J.
TITLE OF INVENTION: NANBV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590

FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hardin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELEPHONE: (508) 359-3876
TELEFAX: (508) 359-3885
INFORMATION FOR SEQ ID NO: 659:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-659

Query Match 50.0%; Score 21; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTERLY 6
| | | | |
Db 1 LTERLY 6

RESULT 9
US-08-390-353A-9
Sequence 9, Application US/08390353A
Patent No. 6107457
GENERAL INFORMATION:
APPLICANT: Arlinghaus, Ralph B.
APPLICANT: Liu, Jiaxin
APPLICANT: Lu, Dia
APPLICANT: Lopez-Berestein, Gabriel
TITLE OF INVENTION: Bcr-Abl Directed Compositions and Uses for
Regulating Philadelphia Chromosome Stimulated
TITLE OF INVENTION: Cell Activity
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,353A
FILING DATE: 16-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: US/SC:421/MAY
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELLEX: N/A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-353A-9

Query Match 47.6%; Score 20; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 KXSP 8
: |||
Db 1 RYSP 5

RESULT 10
US-09-371-710-48
; Sequence 48, Application US/09371710A
; Patent No. 6146868
; GENERAL INFORMATION:
; APPLICANT: Kozel, Thomas R.
; APPLICANT: Bloomer, Sherri L.
; APPLICANT: Savoy, Anne C.
; TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of
; TITLE OF INVENTION: Cryptococcus neoformans and Uses Thereof
; FILE REFERENCE: D6245
; CURRENT APPLICATION NUMBER: US/09/371,710A
; CURRENT FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 48
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: associated amino acid sequence of PCR primer 34-mer
US-09-371-710-48

Query Match 47.6%; Score 20; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 KXSP 8
: |||
Db 2 KYAP 5

RESULT 11
US-09-147-933-31
; Sequence 31, Application US/09147933A
; Patent No. 6168917
; GENERAL INFORMATION:
; APPLICANT: Kilpatrick, David
; TITLE OF INVENTION: DETECTION AND IDENTIFICATION OF
; TITLE OF INVENTION: NON-POLIO ENTEROVIRUSES
; FILE REFERENCE: 62242/US
; CURRENT APPLICATION NUMBER: US/09/147,933A
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: PCT/US97/17734
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: U. S. 60/027,353
; EARLIER FILING DATE: 1996-10-02
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-147-933-31

Query Match 47.6%; Score 20; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.6e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LTKKTS 7

Db 1 ITRRYT 7
: |||

RESULT 12
US-08-862-124-23
; Sequence 23, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-862-124-23

Query Match 47.6%; Score 20; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 KXSP 8
: |||
Db 3 RYSP 6

RESULT 13
US-08-862-124-26
; Sequence 26, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO.: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-862-124-26

Query Match 47.6%; Score 20; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KYSP 8
Db 3 KYSP 6

RESULT 14
US-09-648-386-48
Sequence 48, Application US/09648386
Patent No. 6284508
GENERAL INFORMATION:
APPLICANT: Kozel, Thomas R.
APPLICANT: Bloomer, Sheri L.
APPLICANT: Savoy, Anne C.
TITLE OF INVENTION: Glucuronoxylomannan (GXM)-O-Acetylhydrolase of
FILE REFERENCE: D6245D
CURRENT APPLICATION NUMBER: US/09/648,386
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US 09/371,710
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ. ID NOS: 50
SEQ. ID NO 48
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: associated amino acid sequence of PCR primer 34-mer
US-09-648-386-48

Query Match 47.6%; Score 20; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KYSP 8
Db 2 KYAP 5

RESULT 15
US-08-178-570-47
Sequence 47, Application US/08178570
Patent No. 5532167
GENERAL INFORMATION:
APPLICANT: Lewis C. Cantley
APPLICANT: Zhou Song Yang
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAIVE & COCKFIELD
STREET: 60 STATE STREET, suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1675
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,570
FILING DATE: JANUARY 7, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DeContri, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO.: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-178-570-47

Query Match 47.6%; Score 20; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKKYSP 8
Db 1 EEEYMP 6

Search completed: January 17, 2002, 12:16:07
Job time: 112 sec